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RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/912,436

DATE: 08/02/2001
TIME: 10:45:33

Input Set : A:\48929sequence.app
Output Set: N:\CRF3\08022001\I912436.raw

3 <110> APPLICANT: JELTSCH, Markku M
 4 ALITALO, Kari
 5 OLOFSSON, Birgitta
 6 ERIKSSON, Ulf
 8 <120> TITLE OF INVENTION: GLYCOSYLATED VEGF-B AND METHOD FOR INCEREASING THE
 9 AMOUNT OF SOLUBLE VEGF-B
 11 <130> FILE REFERENCE: 1064-48929PV Markku JELTSCH et al
 C--> 13 <140> CURRENT APPLICATION NUMBER: US/09/912,436
 C--> 14 <141> CURRENT FILING DATE: 2001-07-26
 16 <160> NUMBER OF SEQ ID NOS: 17
 18 <170> SOFTWARE: PatentIn Ver. 2.0
 20 <210> SEQ ID NO: 1
 21 <211> LENGTH: 567
 22 <212> TYPE: DNA
 23 <213> ORGANISM: Homo sapiens
 25 <220> FEATURE:
 26 <221> NAME/KEY: CDS
 27 <222> LOCATION: (1)..(567)
 29 <220> FEATURE:
 30 <221> NAME/KEY: mat_peptide
 31 <222> LOCATION: (64)..(564)
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 36 -20 -15 -10
 38 gcc ccc gcc cag gcc cct gtc tcc cag cct gat gcc cct ggc cac cag 96
 39 Ala Pro Ala Gln Ala Pro Val Ser Gln Pro Asp Ala Pro Gly His Gln
 40 -5 -1 1 5 10
 42 agg aaa gtg gtg tca tgg ata gat gtg tat act cgc gct acc tgc cag 144
 43 Arg Lys Val Val Ser Trp Ile Asp Val Tyr Thr Arg Ala Thr Cys Gln
 44 15 20 25
 46 ccc cgg gag gtg gtg ccc ttg act gtg gag ctc atg ggc acc gtg 192
 47 Pro Arg Glu Val Val Val Pro Leu Thr Val Glu Leu Met Gly Thr Val
 48 30 35 40
 50 gcc aaa cag ctg gtg ccc agc tgc gtg act gtg cag cgc tgt ggt ggc 240
 51 Ala Lys Gln Leu Val Pro Ser Cys Val Thr Val Gln Arg Cys Gly Gly
 52 45 50 55
 54 tgc tgc cct gac gat ggc ctg gag tgt gtg ccc act ggg cag cac caa 288
 55 Cys Cys Pro Asp Asp Gly Leu Glu Cys Val Pro Thr Gly Gln His Gln
 56 60 65 70 75
 58 gtc cgg atg cag atc ctc atg atc cgg tac ccg agc agt cag ctg ggg 336
 59 Val Arg Met Gln Ile Leu Met Ile Arg Tyr Pro Ser Ser Gln Leu Gly
 60 80 85 90
 62 gag atg tcc ctg gaa gaa cac agc cag tgt gaa tgc aga cct aaa aaa 384
 63 Glu Met Ser Leu Glu Glu His Ser Gln Cys Glu Cys Arg Pro Lys Lys
 64 95 100 105
 66 aag gac agt gct gtg aag cca gac agc ccc agg ccc ctc tgc cca cgc 432

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67 Lys Asp Ser Ala Val Lys Pro Asp Ser Pro Arg Pro Leu Cys Pro Arg
68 110 115 120
70 tgc acc cag cac cac cag cgc cct gac ccc cgg acc tgc cgc tgc cgc 480
71 Cys Thr Gln His His Gln Arg Pro Asp Pro Arg Thr Cys Arg Cys Arg
72 125 130 135
74 tgc cga cgc cgc agc ttc ctc cgt tgc caa ggg cgg ggc tta gag ctc 528
75 Cys Arg Arg Arg Ser Phe Leu Arg Cys Gln Gly Arg Gly Leu Glu Leu
76 140 145 150 155
78 aac cca gac acc tgc agg tgc cgg aag ctg cga agg tga 567
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80 160 165
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86 <213> ORGANISM: Homo sapiens
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90 1 5 10 15
92 Ala Pro Ala Gln Ala Pro Val Ser Gln Pro Asp Ala Pro Gly His Gln
93 20 25 30
95 Arg Lys Val Val Ser Trp Ile Asp Val Tyr Thr Arg Ala Thr Cys Gln
96 35 40 45
98 Pro Arg Glu Val Val Val Pro Leu Thr Val Glu Leu Met Gly Thr Val
99 50 55 60
101 Ala Lys Gln Leu Val Pro Ser Cys Val Thr Val Gln Arg Cys Gly Gly
102 65 70 75 80
104 Cys Cys Pro Asp Asp Gly Leu Glu Cys Val Pro Thr Gly Gln His Gln
105 85 90 95
107 Val Arg Met Gln Ile Leu Met Ile Arg Tyr Pro Ser Ser Gln Leu Gly
108 100 105 110
110 Glu Met Ser Leu Glu Glu His Ser Gln Cys Glu Cys Arg Pro Lys Lys
111 115 120 125
113 Lys Asp Ser Ala Val Lys Pro Asp Ser Pro Arg Pro Leu Cys Pro Arg
114 130 135 140
116 Cys Thr Gln His His Gln Arg Pro Asp Pro Arg Thr Cys Arg Cys Arg
117 145 150 155 160
119 Cys Arg Arg Arg Ser Phe Leu Arg Cys Gln Gly Arg Gly Leu Glu Leu
120 165 170 175
122 Asn Pro Asp Thr Cys Arg Cys Arg Lys Leu Arg Arg
123 180 185
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127 <211> LENGTH: 624
128 <212> TYPE: DNA
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132 <221> NAME/KEY: CDS
133 <222> LOCATION: (1)..(621)
135 <220> FEATURE:
136 <221> NAME/KEY: mat_peptide

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137 <222> LOCATION: (64)..(621)
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 142 -20 -15 -10
 144 gcc ccc gcc cag gcc cct gtc tcc cag cct gat gcc cct ggc cac cag 96
 145 Ala Pro Ala Gln Ala Pro Val Ser Gln Pro Asp Ala Pro Gly His Gln
 146 -5 -1 1 5 10
 148 agg aaa gtg gtg tca tgg ata gat gtg tat act cgc gct acc tgc cag 144
 149 Arg Lys Val Val Ser Trp Ile Asp Val Tyr Thr Arg Ala Thr Cys Gln
 150 15 20 25
 152 ccc cgg gag gtg gtg ccc ttg act gtg gag ctc atg ggc acc gtg 192
 153 Pro Arg Glu Val Val Val Pro Leu Thr Val Glu Leu Met Gly Thr Val
 154 30 35 40
 156 gcc aaa cag ctg gtg ccc agc tgc gtg act gtg cag cgc tgt ggt ggc 240
 157 Ala Lys Gln Leu Val Pro Ser Cys Val Thr Val Gln Arg Cys Gly Gly
 158 45 50 55
 160 tgc tgc cct gac gat ggc ctg gag tgt gtg ccc act ggg cag cac caa 288
 161 Cys Cys Pro Asp Asp Gly Leu Glu Cys Val Pro Thr Gly Gln His Gln
 162 60 65 70 75
 164 gtc cgg atg cag atc ctc atg atc cgg tac ccg agc agt cag ctg ggg 336
 165 Val Arg Met Gln Ile Leu Met Ile Arg Tyr Pro Ser Ser Gln Leu Gly
 166 80 85 90
 168 gag atg tcc ctg gaa gaa cac agc cag tgt gaa tgc aga cct aaa aaa 384
 169 Glu Met Ser Leu Glu Glu His Ser Gln Cys Glu Cys Arg Pro Lys Lys
 170 95 100 105
 172 aag gac agt gct gtg aag cca gac agg gct gcc act ccc cac cac cgt 432
 173 Lys Asp Ser Ala Val Lys Pro Asp Arg Ala Ala Thr Pro His His Arg
 174 110 115 120
 176 ccc cag ccc cgt tct gtt ccg ggc tgg gac tct gcc ccc gga gca ccc 480
 177 Pro Gln Pro Arg Ser Val Pro Gly Trp Asp Ser Ala Pro Gly Ala Pro
 178 125 130 135
 180 tcc cca gct gac atc acc cat ccc act cca gcc cca ggc ccc tct gcc 528
 181 Ser Pro Ala Asp Ile Thr His Pro Thr Pro Ala Pro Gly Pro Ser Ala
 182 140 145 150 155
 184 cac gct gca ccc agc acc acc agc gcc ctg acc ccc gga cct gcc gcc 576
 185 His Ala Ala Pro Ser Thr Thr Ser Ala Leu Thr Pro Gly Pro Ala Ala
 186 160 165 170
 188 gcc gct gcc gac gcc gca gct tcc tcc gtt gcc aag ggc ggg gct tag 624
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 190 175 180 185
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 194 <211> LENGTH: 207
 195 <212> TYPE: PRT
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 200 -20 -15 -10
 202 Ala Pro Ala Gln Ala Pro Val Ser Gln Pro Asp Ala Pro Gly His Gln

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205	Arg	Lys	Val	Val	Ser	Trp	Ile	Asp	Val	Tyr	Thr	Arg	Ala	Thr	Cys	Gln
206																
208	Pro	Arg	Glu	Val	Val	Val	Pro	Leu	Thr	Val	Glu	Leu	Met	Gly	Thr	Val
209																
211	Ala	Lys	Gln	Leu	Val	Pro	Ser	Cys	Val	Thr	Val	Gln	Arg	Cys	Gly	Gly
212																
214	Cys	Cys	Pro	Asp	Asp	Gly	Leu	Glu	Cys	Val	Pro	Thr	Gly	Gln	His	Gln
215																
217	Val	Arg	Met	Gln	Ile	Leu	Met	Ile	Arg	Tyr	Pro	Ser	Ser	Gln	Leu	Gly
218																
220	Glu	Met	Ser	Leu	Glu	Glu	His	Ser	Gln	Cys	Glu	Cys	Arg	Pro	Lys	Lys
221																
223	Lys	Asp	Ser	Ala	Val	Lys	Pro	Asp	Arg	Ala	Ala	Thr	Pro	His	His	Arg
224																
226	Pro	Gln	Pro	Arg	Ser	Val	Pro	Gly	Trp	Asp	Ser	Ala	Pro	Gly	Ala	Pro
227																
229	Ser	Pro	Ala	Asp	Ile	Thr	His	Pro	Thr	Pro	Ala	Pro	Gly	Pro	Ser	Ala
230																
232	His	Ala	Ala	Pro	Ser	Thr	Thr	Ser	Ala	Leu	Thr	Pro	Gly	Pro	Ala	Ala
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235	Ala	Ala	Ala	Asp	Ala	Ala	Ser	Ser	Val	Ala	Lys	Gly	Gly	Ala		
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254	Met	Ser	Pro	Leu	Leu	Arg	Arg	Leu	Leu	Leu	Ala	Ala	Leu	Leu	Gln	Leu
255																
257	gcc	ccc	gcc	cag	gcc	cct	gtc	tcc	cag	cct	gat	gcc	cct	ggc	cac	cag
258	Ala	Pro	Ala	Gln	Ala	Pro	Val	Ser	Gln	Pro	Asp	Ala	Pro	Gly	His	Gln
259																
261	agg	aaa	gtg	gtg	tca	tgg	ata	gat	gtg	tat	act	cgc	gct	acc	tgc	cag
262	Arg	Lys	Val	Val	Ser	Trp	Ile	Asp	Val	Tyr	Thr	Arg	Ala	Thr	Cys	Gln
263																
265	ccc	cgg	gag	gtg	gtg	ccc	ttg	act	gtg	gag	ctc	atg	ggc	acc	gtg	
266	Pro	Arg	Glu	Val	Val	Val	Pro	Leu	Thr	Val	Glu	Leu	Met	Gly	Thr	Val
267																
269	gcc	aaa	cag	ctg	gtg	ccc	agc	tgc	gtg	act	gtg	cag	cgc	tgt	ggt	ggc
270	Ala	Lys	Gln	Leu	Val	Pro	Ser	Cys	Val	Thr	Val	Gln	Arg	Cys	Gly	Gly
271																

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273 tgc tgc cct gac gat ggc ctg gag tgt gtg ccc act ggg cag cac caa 288
 274 Cys Cys Pro Asp Asp Gly Leu Glu Cys Val Pro Thr Gly Gln His Gln
 275 60 65 70 75
 277 gtc cgg atg cag atc ctc atg atc cgg tac ccg agc agt cag ctg ggg 336
 278 Val Arg Met Gln Ile Leu Met Ile Arg Tyr Pro Ser Ser Gln Leu Gly
 279 80 85 90
 281 gag atg tcc ctg gaa gaa cac agc cag tgt gaa tgc aga cct aaa aaa 384
 282 Glu Met Ser Leu Glu Glu His Ser Gln Cys Glu Cys Arg Pro Lys Lys
 283 95 100 105
 285 aag gac agt gct gtg aag cca gac 408
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 299 Ala Pro Ala Gln Ala Pro Val Ser Gln Pro Asp Ala Pro Gly His Gln
 300 -5 -1 1 5 10
 302 Arg Lys Val Val Ser Trp Ile Asp Val Tyr Thr Arg Ala Thr Cys Gln
 303 15 20 25
 305 Pro Arg Glu Val Val Val Pro Leu Thr Val Glu Leu Met Gly Thr Val
 306 30 35 40
 308 Ala Lys Gln Leu Val Pro Ser Cys Val Thr Val Gln Arg Cys Gly Gly
 309 45 50 55
 311 Cys Cys Pro Asp Asp Gly Leu Glu Cys Val Pro Thr Gly Gln His Gln
 312 60 65 70 75
 314 Val Arg Met Gln Ile Leu Met Ile Arg Tyr Pro Ser Ser Gln Leu Gly
 315 80 85 90
 317 Glu Met Ser Leu Glu Glu His Ser Gln Cys Glu Cys Arg Pro Lys Lys
 318 95 100 105
 320 Lys Asp Ser Ala Val Lys Pro Asp
 321 110 115
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 325 <211> LENGTH: 5614
 326 <212> TYPE: DNA
 327 <213> ORGANISM: Artificial Sequence
 329 <220> FEATURE:
 330 <223> OTHER INFORMATION: Description of Artificial Sequence:
 331 pSecTagA-VEGF-B167-H6
 333 <400> SEQUENCE: 7
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 336 ccgcatagtt aagccagtat ctgctccctg ctttgtgtt ggaggtcgt gagtagtgcg 120
 338 cgagcaaat ttaagctaca acaaggcaag gcttgaccga caattgcatt aagaatctgc 180
 340 tttagggttag gcgtttcgct ctgcttcgcg atgtacgggc cagatatacg cgttgacatt 240
 342 gattattgac tagttattaa tagtaatcaa ttacgggtc attagttcat agccatata 300
 344 tggagttccg cgttacataa cttacggtaa atggcccgcc tggctgaccg cccaaacgacc 360

VERIFICATION SUMMARY

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L:13 M:270 C: Current Application Number differs, Replaced Application Number

L:14 M:271 C: Current Filing Date differs, Replaced Current Filing Date